

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/426,783DATE: 11/10/1999  
TIME: 17:56:04

INPUT SET: S33895.raw

<p><b>This Raw Listing contains the General Information Section and up to the first 5 pages.</b></p>
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## SEQUENCE LISTING

## (1) General Information:

- (i) APPLICANT: Gonsalves, Dennis  
Pang, Sheng-Zhi
- (ii) TITLE OF INVENTION: TOMATO SPOTTED WILT VIRUS
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Nixon Peabody LLP
  - (B) STREET: Clinton Square, P.O. Box 1051
  - (C) CITY: Rochester
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 14603
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/495,484
  - (B) FILING DATE: 27-JAN-1994
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Goldman, Michael L.
  - (B) REGISTRATION NUMBER: 30,727
  - (C) REFERENCE/DOCKET NUMBER: 19603/10303
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (716) 263-1304
  - (B) TELEFAX: (716) 263-1600

## (2) INFORMATION FOR SEQ ID NO:1:

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47 (i) SEQUENCE CHARACTERISTICS:  
48 (A) LENGTH: 25 base pairs  
49 (B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: single  
51 (D) TOPOLOGY: linear  
52  
53 (ii) MOLECULE TYPE: DNA (genomic)  
54  
55  
56  
57  
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
59  
60 AGCAGGCAAA ACTCGCAGAA CTTGC 25  
61  
62 (2) INFORMATION FOR SEQ ID NO:2:  
63  
64 (i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 25 base pairs  
66 (B) TYPE: nucleic acid  
67 (C) STRANDEDNESS: single  
68 (D) TOPOLOGY: linear  
69  
70 (ii) MOLECULE TYPE: DNA (genomic)  
71  
72  
73  
74  
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
76  
77 GCAAGTTCTG CGAGTTTTGC CTGCT 25  
78  
79 (2) INFORMATION FOR SEQ ID NO:3:  
80  
81 (i) SEQUENCE CHARACTERISTICS:  
82 (A) LENGTH: 32 base pairs  
83 (B) TYPE: nucleic acid  
84 (C) STRANDEDNESS: single  
85 (D) TOPOLOGY: linear  
86  
87 (ii) MOLECULE TYPE: DNA (genomic)  
88  
89  
90  
91  
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
93  
94 AGCTAACCAT GGTAAAGCTC ACTAAGGAAA GC 32  
95  
96 (2) INFORMATION FOR SEQ ID NO:4:  
97  
98 (i) SEQUENCE CHARACTERISTICS:  
99 (A) LENGTH: 32 base pairs

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100 (B) TYPE: nucleic acid  
101 (C) STRANDEDNESS: single  
102 (D) TOPOLOGY: linear  
103  
104 (ii) MOLECULE TYPE: DNA (genomic)  
105  
106  
107  
108  
109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
110  
111 AGCATTCCAT GGTTAACACA CTAAGCAAGC AC 32  
112  
113 (2) INFORMATION FOR SEQ ID NO:5:  
114  
115 (i) SEQUENCE CHARACTERISTICS:  
116 (A) LENGTH: 2216 base pairs  
117 (B) TYPE: nucleic acid  
118 (C) STRANDEDNESS: single  
119 (D) TOPOLOGY: linear  
120  
121 (ii) MOLECULE TYPE: DNA (genomic)  
122  
123  
124  
125  
126 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
127  
128 CAAGTTGAAA GCAACAACAG AACTGTAAAT TCTCTTGCG TGAAATCTCT GCTCATGTCA 60  
129  
130 GCAGAAAACA ACATCATGCC TAACTCTCAA GCTTCCACTG ATTCTCATTT CAAGCTGAGC 120  
131  
132 CTCTGGCTAA GGGTTCCAAA GGTTTTGAAG CAGGTTTCCA TTCAGAAATT GTTCAAGGTT 180  
133  
134 GCAGGAGATG AAACAAACAA AACATTTTAT TTATCTATTG CCTGCATTCC AAACCATAAC 240  
135  
136 AGTGTTGAGA CAGCTTTAAA CATTACTGTT ATTTGCAAGC ATCAGCTCCC AATTCGCAAA 300  
137  
138 TGCAAAGCTC CTTTTGAATT ATCAATGATG TTTTCTGATT TAAAGGAGCC TTACAACATT 360  
139  
140 GTTCATGACC CTTCATACCC CAAAGGATCG GTTCCAATGC TCTGGCTCGA AACTCACACA 420  
141  
142 TCTTTGCACA AGTTCTTTGC AACTAACTTG CAAGAAGATG TAATCATCTA CACTTTGAAC 480  
143  
144 AACCTTGAGC TAACTCCTGG AAAGTTAGAT TTAGGTGAAA GAACCTTGAA TTACAGTGAA 540  
145  
146 GATGCCTACA AAAGGAAATA TTTCTTTTCA AAAACACTTG AATGTCTTCC ATCTAACACA 600  
147  
148 CAAACTATGT CTTACTTAGA CAGCATCCAA ATCCCTTCAT GGAAGATAGA CTTTGCCAGA 660  
149  
150 GGAGAAATTA AAATTTCTCC ACAATCTATT TCAGTTGCAA AATCTTTGTT AAAGCTTGAT 720  
151  
152 TTAAGCGGGA TCAAAAAGAA AGAATCTAAG GTTAAGGAAG CGTATGCTTC AGGATCAAAA 780

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153									
154	TAATCTTGCT	TTGTCCAGCT	TTTTCTAATT	ATGTTATGTT	TATTTTCTTT	CTTTACTTAT		840	
155									
156	AATTATTTCT	CTGTTTGTCA	TCTCTTTCAA	ATTCCTCCTG	TCTAGTAGAA	ACCATAAAAA		900	
157									
158	CAAAAAATAA	AAATGAAAAT	AAAATTAAAA	TAAAATAAAA	TCAAAAAATG	AAATAAAAAAC		960	
159									
160	AACAAAAAAT	TAAAAAACGA	AAAACCAAAA	AGACCCGAAA	GGGACCAATT	TGGCCAAATT		1020	
161									
162	TGGGTTTTGT	TTTTGTTTTT	TGTTTTTTGT	TTTTTATTTT	TTATTTTATT	TTTATTTTAT		1080	
163									
164	TTTATTTTTA	TTTTATTTTT	ATTTTATTTA	TTTTTTGTTT	TCGTTGTTTT	TGTTATTTTA		1140	
165									
166	TTATTTATTA	AGCACAACAC	ACAGAAAGCA	AACTTTAATT	AAACACACTT	ATTTAAAATT		1200	
167									
168	TAACACACTA	AGCAAGCACA	AGCAATAAAG	ATAAAGAAAG	CTTTATATAT	TTATAGGCTT		1260	
169									
170	TTTTATAATT	TAACCTACAG	CTGCTTTCAA	GCAAGTCTCG	CGAGTTTTGC	CTGCTTTTTA		1320	
171									
172	ACCCCGAACA	TTTCATAGAA	CTTGTTAAGA	GTTTCACTGT	AATGTTCCAT	AGCAACACTC		1380	
173									
174	CCTTTAGCAT	TAGGATTGCT	GGAGCTAAGT	ATAGCAGCAT	ACTCTTCCC	CTTCTTCACC		1440	
175									
176	TGATCTTCAT	TCATTTCAA	TGCTTTGCTT	TTCAGCACAG	TGCAAACTTT	TCCTAAGGCT		1500	
177									
178	TCCTTGGTGT	CATACTTCTT	TGGGTCGATC	CCGAGGTCCT	TGTATTTTGC	ATCCTGATAT		1560	
179									
180	ATAGCCAAGA	CAACACTGAT	CATCTCAAAG	CTATCAACTG	AAGCAATAAG	AGGTAAGCTA		1620	
181									
182	CCTCCCAGCA	TTATGGCAAG	TCTCACAGAC	TTTGCATCAT	CGAGAGGTAA	TCCATAGGCT		1680	
183									
184	TGAATCAAAG	GATGGGAAGC	AATCTTAGAT	TTGATAGTAT	TGAGATTCTC	AGAATTCCCA		1740	
185									
186	GTTTCTTCAA	CAAGCCTGAC	CCTGATCAAG	CTATCAAGCC	TTCTGAAGGT	CATGTCAGTG		1800	
187									
188	CCTCCAATCC	TGTCTGAAGT	TTTCTTTATG	GTAATTTTAC	CAAAAGTAAA	ATCGCTTTGC		1860	
189									
190	TTAATAACCT	TCATTATGCT	CTGACGATTC	TTTAGGAATG	TCAGACATGA	AATAACGCTC		1920	
191									
192	ATCTTCTTGA	TCTGGTCGAT	GTTTTCCAGA	CAAAAAGTCT	TGAAGTTGAA	TGCTACCAGA		1980	
193									
194	TTCTGATCTT	CCTCAAATC	AAGGTCTTTG	CCTTGTGTCA	ACAAAGCAAC	AATGCTTTCC		2040	
195									
196	TTAGTGAGCT	TAACCTTAGA	CATGATGATC	GTAAAAGTTG	TTATATGCTT	TGACCGTATG		2100	
197									
198	TAACCTCAAGG	TGCGAAAGTG	CAACTCTGTA	TCCCGCAGTC	GTTTCTTAGG	TTCTTAATGT		2160	
199									
200	GATGATTTGT	AAGACTGAGT	GTTAAGGTAT	GAACACAAAA	TTGACACGAT	TGCTCT			

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/426,783**

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Original Text